



Project title: Investigating durable resistance to *Phytophthora cactorum* in strawberry and apple

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Industry Representative: NA

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The results and conclusions in this report are based on an investigation conducted over a one-year period. The conditions under which the experiments were carried out and the results have been reported in detail and with accuracy. However, because of the biological nature of the work it must be borne in mind that different circumstances and conditions could produce different results. Therefore, care must be taken with interpretation of the results, especially if they are used as the basis for commercial product recommendations.

AUTHENTICATION

We declare that this work was done under our supervision according to the procedures described herein and that the report represents a true and accurate record of the results obtained.

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PhD Student

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Signature Matteo Luberti Date 05/11/2019

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GROWER SUMMARY

Headline

This project aims to identify sources of durable resistance to *Phytophthora cactorum* in strawberry and apple in order to integrate them in the UK breeding programmes.

Background

The genus *Phytophthora* is comprised of a number of pathogenic oomycete (water-mould) species responsible for substantial damages to crops worldwide. *Phytophthora cactorum* can cause disease in over 250 plant hosts, including economically important crops such as cultivated strawberry (*Fragaria x ananassa*) and apple (*Malus x domestica*). *P. cactorum* is homothallic and it can produce both sexual and asexual spores (Erwin and Ribeiro, 1996). The sexual oospores are able to persist in the soil for several decades, while asexual zoospores are bi-flagellate, motile zoospores released in wet conditions which are able to swim towards a suitable host to initiate infection (Khew and Zentmyer, 1973).

P. cactorum is able to cause severe disease (crown and leather rot) in strawberry (Erwin and Ribeiro, 1996). Crown rot infection causes wilting of the plant, usually beginning from the youngest leaves, and red-brown lesions within the crown while leather rot causes the fruit to acquire a “leathery” texture, unpleasant smell and an altered taste resulting in high economic losses. Thus, *P. cactorum* can cause financial loss at all stages of production, from plant propagation all the way to fruit storage. Up to 40% of total strawberry crops were lost in Norway to crown rot (Stensvand *et al.*, 1999) and 20-30% in commercial farms in Ohio due to leather rot (Ellis and Grove, 1983).

Due to the high costs associated with orchard establishment, *P. cactorum* infection can be particularly damaging in perennial plants such as apple and pear (Harris, 1991). Thus, the production of resistant varieties is an important objective in breeding programs. In apple, *P. cactorum* can cause crown, collar and root rot (Erwin and Ribeiro, 1996). It can enter the tree through wounds and it reportedly often initiates infection at the graft union site, producing a moist rot, while below ground the bark tends to turn black and is decomposed by soil microorganisms (Harris, 1991).

Previous work on resistance to *P. cactorum* in strawberry at NIAB EMR has identified three major effect Quantitative Trait Loci (QTL) in a bi-parental cross and additional QTL from a preliminary genome-wide association study (Nellist *et al.*, 2019). In comparison to strawberry where resistance is known to be quantitative, there is very little known about resistance to *P. cactorum* in apple. Although reports exist that suggest the presence of a major resistance

gene in the 'Northern Spy' cultivar (Knight and Alston, 1969), suggesting qualitative resistance. The key deliverables of this project is to identify markers associated with resistance in both strawberry and apple, and to elucidate the underlying molecular plant-pathogen interactions.

Summary

In the first year of this PhD programme, we have screened the UK apple germplasm preserved within NIAB EMR's Genebank for resistance to *P. cactorum*. We focused on genotypes relevant to the rootstock breeding programme, screening 29 varieties. We identified 13 susceptible and nine resistant genotypes, while seven remain inconclusive due to contamination. Using this data, we were able to identify an existing population, M432, available at NIAB EMR which potentially segregates for resistance to *P. cactorum*. We used an excised shoot assay to phenotype the individuals belonging to this population. Using genotypic data previously generated at NIAB EMR, we were subsequently able to perform quantitative trait loci (QTL) mapping. Our analysis identified a major effect resistance QTL responsible for 58.2% of the phenotypic variation observed in the population. Future work will focus on the validation of these results utilising living trees, the identification of the genes responsible for the observed resistance, as well as aiding in the identification of robust markers associated with resistance to be employed in the rootstock breeding programme for the deployment of resistance in the breeding lines. In summary:

- UK apple germplasm genotypes pertinent to the rootstock breeding program were screened using an excised shoot assay in order to identify sources of resistance to *P. cactorum*.
- A major effect resistance QTL was identified using a segregating population phenotyped using the same technique employed in the screen.
- Future work will focus on identifying and characterising the genes responsible for resistance. As well as aiding in the identification of robust markers associated with resistance to be employed in the rootstock breeding programme.
- Future work will aim to identify genes involved in resistance in strawberry by looking at gene expression during plant infection. Using a moderately susceptible (Emily) and a tolerant variety (Fenella), we aim to identify genes that confer resistance.

Financial Benefits

This report summarises the work that has been carried out in the first year of this PhD project. As this is a four-year programme, there are no direct financial benefits to be reported as of

yet. However, the data presented in this annual report is already contributing to the selection of genotypes to be employed in the rootstock breeding programme at NIAB EMR.

Action Points

- There are no action points at this early stage of the project.

